

SEQUENCE LISTING

5 <110> Regents of the University of Minnesota et al.
 <120> Streptococcal C5a peptidase vaccine
 <130> 600.450WO1
 10 <150> US 09/206,898
 <151> 1998-12-07
 <150> US 08/589,756
 <151> 1996-01-22
 15 <160> 23
 <170> FastSEQ for Windows Version 3.0
 20 <210> 1
 <211> 1164
 <212> PRT
 <213> Streptococcus pyogenes
 25 <400> 1
 Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
 1 5 10 15
 Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
 20 25 30
 30 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Thr Pro
 35 40 45
 Gln Pro Thr Thr Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys
 50 55 60
 Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Val Ala Asp Asp Ala
 35 65 70 75 80
 Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Pro Asp Thr Ser Ala
 85 90 95
 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
 100 105 110
 40 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
 115 120 125

B1 "SEQUENCE LISTING"

THE 1990S

Asn Ser Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
 450 455 460
 Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
 465 470 475 480
 5 Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
 485 490 495
 Leu Ser Ser Ala Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
 500 505 510
 Met Ser Ala Pro Leu Val Ala Val Ile Met Gly Leu Leu Gln Lys Gln
 10 515 520 525
 Tyr Glu Thr Gln Tyr Pro Asp Met Thr Gln Ser Glu Arg Leu Asp Leu
 530 535 540
 Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
 545 550 555 560
 15 Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
 565 570 575
 Ala Lys Lys Ala Ser Glu Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
 580 585 590
 Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
 20 595 600 605
 Thr Val Thr Val His Asn Lys Ser Asp Lys Pro His Glu Leu Tyr Tyr
 610 615 620
 Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
 625 630 635 640
 25 Ala Pro Lys Ala Leu Ile Glu Thr Ser Trp Gln Lys Ile Thr Ile Pro
 645 650 655
 Ala Asn Ser Ser Lys Gln Val Thr Ile Pro Ile Asp Ile Ser Gln Phe
 660 665 670
 Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
 30 675 680 685
 Phe Val Arg Ile Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
 690 695 700
 Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
 705 710 715 720
 35 Lys Pro Leu Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Glu
 725 730 735
 Ile Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
 740 745 750
 Ala Leu Lys Asn Asp Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
 40 755 760 765

B1

PCT/US99/28826

	Thr	Ile	Asn	Val	Val	Lys	Glu	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile	
	770					775				780						
	Glu	Ser	Ser	Glu	Ile	Thr	Glu	Thr	Ile	Phe	Ala	Gly	Thr	Phe	Ala	Lys
	785					790				795						800
5	Gln	Asp	Asp	Asp	Arg	His	Tyr	Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Lys
					805					810					815	
	Pro	Tyr	Ala	Ala	Ile	Ser	Pro	Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val
					820					825				830		
	Gln	Phe	His	Gly	Thr	Phe	Leu	Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu
10		835						840					845			
	Val	Leu	Asp	Lys	Glu	Gly	Asn	Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu
	850						855					860				
	Gln	Val	Val	Lys	Asn	Tyr	Asn	Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser
	865				870					875						880
15	Thr	Arg	Phe	Glu	Ile	Ser	Arg	Trp	Asp	Gly	Lys	Asp	Lys	Asp	Ala	Lys
					885					890					895	
	Val	Val	Ala	Asn	Gly	Thr	Tyr	Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile
					900					905				910		
	Ser	Ser	Gly	Ala	Lys	Glu	Gln	His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp
20		915						920					925			
	Asn	Thr	Thr	Pro	Glu	Val	Ala	Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp
	930						935					940				
	Arg	Arg	Leu	Thr	Leu	Ala	Ser	Lys	Pro	Gln	Thr	Ser	Gln	Pro	Val	Tyr
	945				950					955						960
25	Arg	Glu	Arg	Ile	Ala	Tyr	Thr	Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr
					965					970					975	
	Glu	Tyr	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu
					980					985				990		
	Ala	Glu	Thr	Met	Glu	Gly	Ala	Thr	Val	Pro	Leu	Lys	Met	Ser	Asp	Phe
30		995						1000					1005			
	Thr	Tyr	Val	Val	Glu	Asp	Met	Ala	Gly	Asn	Ile	Thr	Tyr	Thr	Pro	Val
	1010						1015					1020				
	Thr	Lys	Leu	Leu	Glu	Gly	His	Ser	Asn	Lys	Pro	Glu	Gln	Asp	Gly	Ser
	1025				1030					1035						1040
35	Asp	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Thr	Lys	Pro	Glu			

[illegible]

[illegible][illegible]

	500					505					510					
	Met	Ser	Ala	Pro	Leu	Val	Ala	Gly	Ile	Met	Gly	Leu	Leu	Gln	Lys	Gln
	515					520					525					
	Tyr	Glu	Thr	Gln	Tyr	Pro	Asp	Met	Thr	Pro	Ser	Glu	Arg	Leu	Asp	Leu
5	530					535					540					
	Ala	Lys	Lys	Val	Leu	Met	Ser	Ser	Ala	Thr	Ala	Leu	Tyr	Asp	Glu	Asp
	545					550					555					560
	Glu	Lys	Ala	Tyr	Phe	Ser	Pro	Arg	Gln	Gln	Gly	Ala	Gly	Ala	Val	Asp
	565					570					575					
10	Ala	Lys	Lys	Ala	Ser	Ala	Ala	Thr	Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn
	580					585					590					
	Thr	Ser	Ser	Lys	Val	His	Leu	Asn	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val
	595					600					605					
	Thr	Val	Thr	Val	His	Asn	Lys	Ser	Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr
15	610					615					620					
	Gln	Ala	Thr	Val	Gln	Thr	Asp	Lys	Val	Asp	Gly	Lys	His	Phe	Ala	Leu
	625					630					635					640
	Ala	Pro	Lys	Val	Leu	Tyr	Glu	Ala	Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro
	645					650					655					
20	Ala	Asn	Ser	Ser	Lys	Gln	Val	Thr	Val	Pro	Ile	Asp	Ala	Ser	Arg	Phe
	660					665					670					
	Ser	Lys	Asp	Leu	Leu	Ala	Gln	Met	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly
	675					680					685					
	Phe	Val	Arg	Phe	Lys	Gln	Asp	Pro	Thr	Lys	Glu	Glu	Leu	Met	Ser	Ile
25	690					695					700					
	Pro	Tyr	Ile	Gly	Phe	Arg	Gly	Asp	Phe	Gly	Asn	Leu	Ser	Ala	Val	Glu
	705					710					715					720
	Lys	Pro	Ile	Tyr	Asp	Ser	Lys	Asp	Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala
	725					730					735					
30	Asn	Ser	Asp	Ala	Lys	Asp	Gln	Leu	Asp	Gly	Asp	Gly	Leu	Gln	Phe	Tyr
	740					745					750					
	Ala	Leu	Lys	Asn	Asn	Phe	Thr	Ala	Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp
	755					760					765					
	Thr	Ile	Ile	Lys	Ala	Val	Lys	Glu	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile
35	770					775					780					
	Glu	Ser	Ser	Glu	Ile	Thr	Glu	Thr	Ile	Phe	Ala	Gly	Thr	Phe	Ala	Lys
	785					790					795					800
	Gln	Asp	Asp	Asp	Ser	His	Tyr	Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Glu
	805					810					815					
40	Pro	Tyr	Ala	Ala	Ile	Ser	Pro	Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

	820	825	830
	Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu		
	835	840	845
	Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu		
5	850	855	860
	Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser		
	865	870	875 880
	Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys		
	885	890	895
10	Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile		
	900	905	910
	Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp		
	915	920	925
	Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp		
15	930	935	940
	Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr		
	945	950	955 960
	Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr		
	965	970	975
20	Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu		
	980	985	990
	Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe		
	995	1000	1005
	Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val		
25	1010	1015	1020
	Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser		
	1025	1030	1035 1040
	Gly Gln Thr Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp Gly		
	1045	1050	1055
30	Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp		
	1060	1065	1070
	Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys		
	1075	1080	1085
	Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro		
35	1090	1095	1100
	Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys		
	1105	1110	1115 1120
	Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn		
	1125	1130	1135
40	Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Phe Gly Leu		

1140 1145 1150
 Val Ala His Ile Phe Lys Thr Lys Arg Gln Lys Glu Thr Lys Lys
 1155 1160 1165
 5 <210> 3
 <211> 1150
 <212> PRT
 <213> Streptococcus agalactiae
 10 <400> 3
 Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
 1 5 10 15
 Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
 20 25 30
 15 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Thr Val Glu Thr Pro
 35 40 45
 Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys
 50 55 60
 Thr Pro Gln Thr Pro Ser Asp Ala Gly Glu Thr Val Ala Asp Asp Ala
 20 65 70 75 80
 Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
 85 90 95
 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
 100 105 110
 25 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
 115 120 125
 Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
 130 135 140
 Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
 30 145 150 155 160
 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
 165 170 175
 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
 180 185 190
 35 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
 195 200 205
 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
 210 215 220
 Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
 40 225 230 235 240

B1

 1140 1145 1150
 1155 1160 1165
 1170 1175 1180
 1185 1190 1195
 1200 1205 1210
 1215 1220 1225
 1230 1235 1240
 1245 1250 1255
 1260 1265 1270
 1275 1280 1285
 1290 1295 1300
 1305 1310 1315
 1320 1325 1330
 1335 1340 1345
 1350 1355 1360
 1365 1370 1375
 1380 1385 1390
 1395 1400 1405
 1410 1415 1420
 1425 1430 1435
 1440 1445 1450
 1455 1460 1465
 1470 1475 1480
 1485 1490 1495
 1500 1505 1510
 1515 1520 1525
 1530 1535 1540
 1545 1550 1555
 1560 1565 1570
 1575 1580 1585
 1590 1595 1600
 1605 1610 1615
 1620 1625 1630
 1635 1640 1645
 1650 1655 1660
 1665 1670 1675
 1680 1685 1690
 1695 1700 1705
 1710 1715 1720
 1725 1730 1735
 1740 1745 1750
 1755 1760 1765
 1770 1775 1780
 1785 1790 1795
 1800 1805 1810
 1815 1820 1825
 1830 1835 1840
 1845 1850 1855
 1860 1865 1870
 1875 1880 1885
 1890 1895 1900
 1905 1910 1915
 1920 1925 1930
 1935 1940 1945
 1950 1955 1960
 1965 1970 1975
 1980 1985 1990
 1995 2000 2005
 2010 2015 2020
 2025 2030 2035
 2040 2045 2050
 2055 2060 2065
 2070 2075 2080
 2085 2090 2095
 2100 2105 2110
 2115 2120 2125
 2130 2135 2140
 2145 2150 2155
 2160 2165 2170
 2175 2180 2185
 2190 2195 2200
 2205 2210 2215
 2220 2225 2230
 2235 2240 2245
 2250 2255 2260
 2265 2270 2275
 2280 2285 2290
 2295 2300 2305
 2310 2315 2320
 2325 2330 2335
 2340 2345 2350
 2355 2360 2365
 2370 2375 2380
 2385 2390 2395
 2400 2405 2410
 2415 2420 2425
 2430 2435 2440
 2445 2450 2455
 2460 2465 2470
 2475 2480 2485
 2490 2495 2500

10

Asn Tyr Ala Gln Ala Ile Arg Asp Ala Ile Asn Leu Gly Ala Lys Val
 245 250 255
 Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
 260 265 270
 5 Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
 275 280 285
 Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
 290 295 300
 Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
 10 305 310 315 320
 Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
 325 330 335
 Leu Thr Glu Thr Val Arg Val Lys Thr Ala Asp Gln Gln Asp Lys Glu
 340 345 350
 15 Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
 355 360 365
 Tyr Ala Tyr Ala Asn Arg Gly Thr Lys Glu Asp Asp Phe Lys Asp Val
 370 375 380
 Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp
 20 385 390 395 400
 Lys Ile Ala Lys Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
 405 410 415
 Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
 420 425 430
 25 Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
 435 440 445
 Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
 450 455 460
 Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
 30 465 470 475 480
 Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
 485 490 495
 Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
 500 505 510
 35 Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
 515 520 525
 Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
 530 535 540
 Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
 40 545 550 555 560

B1

PCT/US99/28826

	Glu	Lys	Ala	Tyr	Phe	Ser	Pro	Arg	Gln	Gly	Ala	Gly	Ala	Val	Asp	
					565					570					575	
	Ala	Lys	Lys	Ala	Ser	Ala	Ala	Thr	Met	Tyr	Val	Thr	Asp	Lys	Asp	Asn
				580					585					590		
5	Thr	Ser	Ser	Lys	Val	His	Leu	Asn	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val
				595				600					605			
	Thr	Val	Asn	Val	His	Asn	Lys	Ser	Asp	Lys	Pro	Gln	Glu	Leu	Tyr	Tyr
		610					615					620				
	Gln	Ala	Thr	Val	Gln	Thr	Asp	Lys	Val	Asp	Gly	Lys	His	Phe	Ala	Leu
10	625					630					635					640
	Ala	Pro	Lys	Val	Leu	Tyr	Glu	Ala	Ser	Trp	Gln	Lys	Ile	Thr	Ile	Pro
				645						650					655	
	Ala	Asn	Ser	Ser	Lys	Gln	Val	Thr	Val	Pro	Ile	Asp	Ala	Ser	Arg	Phe
				660					665					670		
15	Ser	Lys	Asp	Leu	Leu	Ala	Gln	Met	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly
			675					680					685			
	Phe	Val	Arg	Phe	Lys	Gln	Asp	Pro	Lys	Lys	Glu	Glu	Leu	Met	Ser	Ile
		690					695					700				
	Pro	Tyr	Ile	Gly	Phe	Arg	Gly	Asp	Phe	Gly	Asn	Leu	Ser	Ala	Leu	Glu
20	705					710					715					720
	Lys	Pro	Ile	Tyr	Asp	Ser	Lys	Asp	Gly	Ser	Ser	Tyr	Tyr	His	Glu	Ala
				725						730					735	
	Asn	Ser	Asp	Ala	Lys	Asp	Gln	Leu	Asp	Gly	Asp	Gly	Leu	Gln	Phe	Tyr
				740					745					750		
25	Ala	Leu	Lys	Asn	Asn	Phe	Thr	Ala	Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp
			755					760					765			
	Thr	Ile	Ile	Lys	Ala	Val	Lys	Glu	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile
		770					775					780				
	Glu	Ser	Ser	Glu	Ile	Thr	Glu	Thr	Ile	Leu	Ala	Gly	Thr	Phe	Ala	Lys
30	785					790					795					800
	Gln	Asp	Asp	Asp	Ser	His	Tyr	Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Lys
				805						810					815	
	Pro	Tyr	Ala	Ala	Ile	Ser	Pro	Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val
				820					825					830		
35	Gln	Phe	Gln	Gly	Thr	Phe	Leu	Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu
			835					840					845			
	Val	Leu	Asp	Lys	Glu	Gly	Asn	Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu
		850					855					860				
	Gln	Val	Val	Lys	Asn	Tyr	Asn	Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser
40	865					870						875				880

	Thr	Arg	Phe	Glu	Lys	Thr	Arg	Trp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys
					885					890						895
	Val	Val	Ala	Asn	Gly	Thr	Tyr	Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile
				900					905					910		
5	Ser	Ser	Gly	Ala	Lys	Glu	Gln	His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp
			915					920					925			
	Asn	Thr	Thr	Pro	Glu	Val	Ala	Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp
			930				935					940				
	Arg	Arg	Leu	Thr	Leu	Ala	Ser	Lys	Pro	Lys	Thr	Ser	Gln	Pro	Val	Tyr
10	945					950					955					960
	Arg	Glu	Arg	Ile	Ala	Tyr	Thr	Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr
				965						970					975	
	Glu	Tyr	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu
				980					985					990		
15	Ala	Glu	Thr	Thr	Glu	Gly	Ala	Thr	Val	Pro	Leu	Lys	Met	Ser	Asp	Phe
			995					1000					1005			
	Thr	Tyr	Val	Val	Glu	Asp	Met	Ala	Gly	Asn	Ile	Thr	Tyr	Thr	Pro	Val
			1010				1015						1020			
	Thr	Lys	Leu	Leu	Glu	Gly	His	Ser	Asn	Lys	Pro	Glu	Gln	Asp	Gly	Ser
20	1025					1030					1035					1040
	Asp	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Ala	Lys	Pro	Glu	Gln	Asp	Gly
				1045						1050					1055	
	Ser	Gly	Gln	Thr	Pro	Asp	Lys	Lys	Thr	Glu	Thr	Lys	Pro	Glu	Lys	Asp
				1060					1065					1070		
25	Ser	Ser	Gly	Gln	Thr	Pro	Gly	Lys	Thr	Pro	Gln	Lys	Gly	Gln	Pro	Ser
			1075					1080					1085			
	Arg	Thr	Leu	Glu	Lys	Arg	Ser	Ser	Lys	Arg	Ala	Leu	Ala	Thr	Lys	Ala
			1090				1095					1100				
	Ser	Thr	Arg	Asp	Gln	Leu	Pro	Thr	Thr	Asn	Asp	Lys	Asp	Thr	Asn	Arg
30	1105					1110					1115					1120
	Leu	His	Leu	Leu	Lys	Leu	Val	Met	Thr	Thr	Phe	Phe	Leu	Gly	Leu	Val
				1125						1130					1135	
	Ala	His	Ile	Phe	Lys	Thr	Lys	Arg	Gln	Lys	Glu	Thr	Lys	Lys		
				1140					1145					1150		

```
<210> 4
<211> 31
<212> DNA
<213> Streptococcus pyogenes
```

13

<400> 4

gggggggaat tcgtagcggg tatcatggga c

31

<210> 5

5 <211> 31

<212> DNA

<213> Streptococcus pyogenes

<400> 5

10 ggggggggaat tcgggtgctg caatatctgg c

31

<210> 6

<211> 17

<212> DNA

15 <213> Streptococcus pyogenes

<400> 6

gtaaaacgac ggccagt

17

20 <210> 7

<211> 19

<212> DNA

<213> Streptococcus pyogenes

25 <400> 7

aaggacgaca cattgcgta

19

<210> 8

<211> 31

30 <212> DNA

<213> Streptococcus pyogenes

<400> 8

ccccccggat ccaccaaaac cccacaaact c

31

35

<210> 9

<211> 18

<212> DNA

<213> Streptococcus pyogenes

40

B1

PCT/US99/28826

14

<400> 9

gagtggccct ccaatagc

18

<210> 10

5 <211> 35

<212> DNA

<213> Streptococcus pyogenes

<400> 10

10 ccccccgat ccaatactgt gacagaagac actcc

35

<210> 11

<211> 25

<212> DNA

15 <213> Streptococcus pyogenes

<400> 11

tttctggaac tagtatgtct gcgcc

25

20 <210> 12

<211> 41

<212> DNA

<213> Streptococcus pyogenes

25 <400> 12

ccccccctcg agatgtaaac gatttgatc cttgtcatta g

41

<210> 13

<211> 25

30 <212> DNA

<213> Streptococcus pyogenes

<400> 13

cagtgattga tgctggtttt gataa

25

35

<210> 14

<211> 18

<212> DNA

<213> Streptococcus pyogenes

40

B1

PCT/US99/28826

15

<400> 14

agctactatc agcaccag .

18

<210> 15

5 <211> 38

<212> DNA

<213> Streptococcus pyogenes

<400> 15

10 cccccgaat tcattactgt gacagaagac actcctgc

38

<210> 16

<211> 39

<212> DNA

15 <213> Streptococcus pyogenes

<400> 16

ccccccgat ccttattgtt ctggtttatt agagtggcc

39

20 <210> 17

<211> 33

<212> DNA

<213> Streptococcus pyogenes

25 <400> 17

attgctgctg gttttgataa aaatcatgaa gcg

33

<210> 18

<211> 18

30 <212> DNA

<213> Streptococcus pyogenes

<400> 18

cactgcaaca acagtccc

18

35

<210> 19

<211> 18

<212> DNA

<213> Streptococcus pyogenes

40

B1
PCT/US99/28826

16

<400> 19

gaggccggca cacacgtg

18

<210> 20

5 <211> 21

<212> DNA

<213> Streptococcus pyogenes

<400>. 20

10 ttgatcgaca gcggttttac c

21

<210> 21

<211> 22

<212> DNA

15 <213> Streptococcus pyogenes

<400> 21

actgctatgt ctgctccatt ag

22

20 <210> 22

<211> 31

<212> DNA

<213> Streptococcus pyogenes

25 <400> 22

tccagaaagt ttggcatact tgttgtagc c

31

<210> 23

<211> 118.1

30 <212> PRT

<213> Streptococcus pyogenes

<400> 23

Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
35 1 5 10 15

Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
20 25 30

Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Thr Pro
35 40 45

40 Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys

	50					55						60					
	Thr	Pro	Gln	Thr	Pro	Asp	Asp	Ala	Glu	Glu	Thr	Ile	Ala	Asp	Asp	Ala	
	65					70					75					80	
	Asn	Asp	Leu	Ala	Pro	Gln	Ala	Pro	Ala	Lys	Thr	Ala	Asp	Thr	Pro	Ala	
5					85					90					95		
	Thr	Ser	Lys	Ala	Thr	Ile	Arg	Asp	Leu	Asn	Asp	Pro	Ser	Gln	Val	Lys	
				100					105					110			
	Thr	Leu	Gln	Glu	Lys	Ala	Gly	Lys	Gly	Ala	Gly	Thr	Val	Val	Ala	Val	
			115					120					125				
10	Ile	Asp	Ala	Gly	Phe	Asp	Lys	Asn	His	Glu	Ala	Trp	Arg	Leu	Thr	Asp	
	130						135					140					
	Lys	Thr	Lys	Ala	Arg	Tyr	Gln	Ser	Lys	Glu	Asp	Leu	Glu	Lys	Ala	Lys	
	145					150					155					160	
	Lys	Glu	His	Gly	Ile	Thr	Tyr	Gly	Glu	Trp	Val	Asn	Asp	Lys	Val	Ala	
15					165					170					175		
	Tyr	Tyr	His	Asp	Tyr	Ser	Lys	Asp	Gly	Lys	Thr	Ala	Val	Asp	Gln	Glu	
				180					185					190			
	His	Gly	Thr	His	Val	Ser	Gly	Ile	Leu	Ser	Gly	Asn	Ala	Pro	Ser	Glu	
			195					200					205				
20	Thr	Lys	Glu	Pro	Tyr	Arg	Leu	Glu	Gly	Ala	Met	Pro	Glu	Ala	Gln	Leu	
	210						215					220					
	Leu	Leu	Met	Arg	Val	Glu	Ile	Val	Asn	Gly	Leu	Ala	Asp	Tyr	Ala	Arg	
	225					230					235					240	
	Asn	Tyr	Ala	Gln	Ala	Ile	Ile	Asp	Ala	Val	Asn	Leu	Gly	Ala	Lys	Val	
25					245						250				255		
	Ile	Asn	Met	Ser	Phe	Gly	Asn	Ala	Ala	Leu	Ala	Tyr	Ala	Asn	Leu	Pro	
				260					265					270			
	Asp	Glu	Thr	Lys	Lys	Ala	Phe	Asp	Tyr	Ala	Lys	Ser	Lys	Gly	Val	Ser	
		275						280					285				
30	Ile	Val	Thr	Ser	Ala	Gly	Asn	Asp	Ser	Ser	Phe	Gly	Gly	Lys	Thr	Arg	
	290						295					300					
	Leu	Pro	Leu	Ala	Asp	His	Pro	Asp	Tyr	Gly	Val	Val	Gly	Thr	Pro	Ala	
	305					310					315					320	
	Ala	Ala	Asp	Ser	Thr	Leu	Thr	Val	Ala	Ser	Tyr	Ser	Pro	Asp	Lys	Gln	
35					325						330				335		
	Leu	Thr	Glu	Thr	Ala	Thr	Val	Lys	Thr	Ala	Asp	Gln	Gln	Asp	Lys	Glu	
			340					345					350				
	Met	Pro	Val	Leu	Ser	Thr	Asn	Arg	Phe	Glu	Pro	Asn	Lys	Ala	Tyr	Asp	
		355						360					365				
40	Tyr	Ala	Tyr	Ala	Asn	Arg	Gly	Met	Lys	Glu	Asp	Asp	Phe	Lys	Asp	Val	

	370	375	380
	Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp		
	385	390	395 400
	Lys Ile Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr		
5	405	410	415
	Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln		
	420	425	430
	Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Glu		
	435	440	445
10	Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro		
	450	455	460
	Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr		
	465	470	475 480
	Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile		
15	485	490	495
	Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser		
	500	505	510
	Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln		
	515	520	525
20	Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu		
	530	535	540
	Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp		
	545	550	555 560
	Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp		
25	565	570	575
	Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn		
	580	585	590
	Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val		
	595	600	605
30	Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr		
	610	615	620
	Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys Leu Phe Ala Leu		
	625	630	635 640
	Ala Pro Lys Ala Leu Tyr Glu Ala Ser Trp Gln Lys Ile Thr Ile Pro		
35	645	650	655
	Ala Asn Ser Ser Lys Gln Val Thr Ile Pro Ile Asp Val Ser Gln Phe		
	660	665	670
	Ser Lys Asp Leu Leu Ala Pro Met Lys Asn Gly Tyr Phe Leu Glu Gly		
	675	680	685
40	Phe Val Arg Phe Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile		

B1

[illegible]

20

1010 1015 1020
 Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
 1025 1030 1035 1040
 Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly
 5 1045 1050 1055
 Ser Gly Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp
 1060 1065 1070
 Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln
 1075 1080 1085
 10 Asp Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu
 1090 1095 1100
 Lys Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln
 1105 1110 1115 1120
 Pro Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr
 15 1125 1130 1135
 Lys Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr
 1140 1145 1150
 Asn Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly
 1155 1160 1165
 20 Leu Val Ala His Ile Phe Lys Thr Lys Arg Thr Lys Lys
 1170 1175 1180

B1
 concludes

1100
 1105
 1110
 1115
 1120
 1125
 1130
 1135
 1140
 1145
 1150
 1155
 1160
 1165
 1170
 1175
 1180